

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA A.
COHEN, MAURICE
COLPITTS, TRACEY L.
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HAYDEN, MARK
KLASS, MICHAEL R.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT

(iii) NUMBER OF SEQUENCES: 51

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/829,754
(B) FILING DATE: 31-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6067.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

10840

09049696 032798

84

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAAATCACAG	GGAGATGTAC	AGCAATGGGG	CCATTTAAGA	GTTCTGTGTT	CATCTTGATT	60
CTTCACCTTC	TAGAAGGGGC	CCTGAGTAAT	TCACTCATTC	AGCTGAACAA	CAATGGCTAT	120
GAAGGCATTG	TCGTTGCAAT	CGACCCCAAT	GTGCCAGAAG	ATGAAACACT	CATTCAACAA	180
ATAAAGGACA	TGGTGACCCA	GGCATCTCTG	TATCTGTTTG	AAG		223

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 158
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 221
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 231
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 251
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTGCAATCG	ACCCCAATGT	GCCAGAAGAT	GAAACACTCA	TTCAACAAAT	AAAGGACATG	60
GTGACCCAGG	CATCTCTGTA	TCTGTTTGAA	GCTACAGGAA	AGCGATTTTA	TTTCAAAAAT	120
GTTGCCATTT	TGATTCTTGA	AACATGGAAG	ACAAAGGNTG	ACTATGTGAG	ACCAAACTT	180
GAGACCTACA	AAAATGCTGA	TGTTCTGGTT	GCTGAGTCTA	NTCCTCCAGG	NAATGATGAA	240
CCCTACACTG	NGCAGATGGG	CAACTGTGGC	GAG			273

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AAAATGCTGA	TGTTCTGGTT	GCTGAGTCTA	CTCCTCCAGG	TAATGATGAA	CCCTACACTG	60
AGCAGATGGG	CAACTGTGGA	GAGAAGGGTG	AAAGGATCCA	CCTCACTCCT	GATTTTCATTG	120
CAGGAAAAAA	GTTAGCTGAA	TATGGACCAC	AAGGTAGGGC	ATTGTGCCAT	GAGTGGGCTC	180
ATCTACGATG	GGGAGTATTT	GACGAGTACA	ATAATGATGA	GAAATTCTAC	TTATCCAATG	240

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAAAGATGC	ACATTCAATA	AAGTAACAGG	ACTCTATGAA	AAAGGATGTG	AGTTTGTTCT	60
CCAATCCCGC	CAGACGGAGA	AGGCTTCTAT	AATGTTTGCA	CAACATGTTG	ATTCTATAGT	120
TGAATTCTGT	ACAGAACAAA	ACCACAACAA	AGAAGCTCCA	AACAAGCAAA	ATCAAAAATG	180
C						181

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTATAGTTGA	ATTCTGTACA	GAACAAAACC	ACAACAAAGA	AGCTCCAAAC	AAGCAAAATC	60
AAAAATGCAA	TCTCCGAAGC	ACATGGGAAG	TGATCCGTGA	TTCTGAGGAC	TTTAAGAAAA	120
CCACTCCTAT	GACAACACAG	CCACCAAATC	CCACCTTCTC	ATTGCTGCAG	ATTGGACAAA	180
GAATTGTGTG	TTTAGTCCTT	GACAAATCTG	GAAGCATGGC			220

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAAGAATTG	TGTGTTTAGT	CCTTGACAAA	TCTGGAAGCA	TGGCGACTGG	TAACCGCCTC	60
AATCGACTGA	ATCAAGCAGG	CCAGCTTTTC	CTGCTGCAGA	CAGTTGAGCT	GGGGTCCTGG	120
GTTGGGATGG	TGACATTTGA	CAGTGCTGCC	CATGTACAAA	GTGAACTCAT	ACAGATAAAC	180
AGTGGCAGTG	ACAGGGACAC	ACTCGCCAAA	AGATTACCTG	CAGCAGCTTC	AGGAGGGACG	240
TCCATCTGCA	GC					252

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 92

86

09049596 032798

(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAATATCCA	ACTGATGGAT	CTGAAATTGT	GCTGCTGACG	GATGGGGAAG	ACAACACTAT	60
AAGTGGGTGC	TTTAACGAGG	TCAAACAAAG	TNGTGCCATC	ATCCACACAG	TCGCTTTGGG	120
GCCCTCTGCA	GCTCAAGAAC	TAGAGGAGCT	GTCCAAAATG	ACAGGAGGTT	TACAGACATA	180
TGCTTCAGAT	CAAGTTCAGA	ACAATGGCCT	CATTGATGCT	TTTGGGGCCC	TTTCATCAGG	240
AAATGGAGCT	GTCTCTCAGC	GCTCCATCCA	GCTTGAGAGT	AAGGGATTA		289

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACAAAGTGG	TGCCATCATC	CACACAGTCG	CTTTGGGGCC	CTCTGCAGCT	CAAGAACTAG	60
AGGAGCTGTC	CAAAATGACA	GGAGGTTTAC	AGACATATGC	TTCAGATCAA	GTTCAGAACA	120
ATGGCCTCAT	TGATGCTTTT	GGGGCCCTTT	CATCAGGAAA	TGGAGCTGTC	TCTCAGCGCT	180
CCATCCAGCT	TGAGAGTAAG	GGATTAACCC	TCCAGAACAG	CCAGTGGATG	AATGGCACAG	240
TGATCGTGGA	CAG					253

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAACAATGGC	CTCATTGATG	CTTTTGGGGC	CCTTTTCATCA	GGAAATGGAG	CTGTCTCTCA	60
GCGCTCCATC	CAGCTTGAGA	GTAAGGGATT	AACCTTCCAG	AACAGCCAGT	GGATGAATGG	120
CACAGTGATC	TGGGACAGCA	CCGTGGGAAA	GGACACTTTG	TTTCTTATCA	CCTGGACAAC	180
GCAGCCTCCC	CAAATCCTTC	TCTGGGATCC	CAGTGGAC			218

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCACAGTGA	TCGTGGACAG	CACCGTGGGA	AAGGACACTT	TGTTTCTTAT	CACCTGGACA	60
ACGCAGCCTC	CCCAAATCCT	TCTCTGGGAT	CCCAGTGGAC	AGAAGCAAGG	TGGCTTTGTA	120
GTGGACAAAA	ACACCAAAAT	GGCCTACCTC	CAAATCCAG	GCATTGCTAA	GGTTGGCACT	180
TGGAAATACA	GTCTGCAAGC	AAGCTCACAA	ACCTTGACCC	TGACTGTCA		229

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

87

09049696 032798

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTTTGTAG	TGGACAAAAA	CACCAAAATG	GCCTACCTCC	AAATCCCAGG	CATTGCTAAG	60
GTTGGCACTT	GGAAATACAG	TCTGCAAGCA	AGCTCACAAA	CCTTGACCCT	GACTGTCACG	120
TCCCGTGCGT	CCAATGCTAC	CCTGCCTCCA	ATTACAGTGA	CTTCCAAAAC	GAACAAGGAC	180
ACCAGCAAAT	T					191

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACACCAGCA	AATTCCCCAG	CCCTCTGGTA	GTTTATGCAA	ATATTCGCCA	AGGAGCCTCC	60
CCAATTCTCA	GGGCCAGTGT	CACAGCCCTG	ATTGAATCAG	TGAATGGAAA	AACAGTTACC	120
TTGGAACACT	TGGATAATGG	AGCAGGTGCT	GATGCTACTA	AGGATGACGG	TGTCTACTCA	180
AGGTATTTC	CAACTTATGA	CACGAATGGT	AGATACAGTG	TAAAAGTGCG	GGCTC	235

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTGCGGGCTC	TGGGAGGAGT	TAACGCAGCC	AGACGGAGAG	TGATACCCCA	GCAGAGTGGA	60
GCACTGTACA	TACCTGGCTG	GATTGAGAAT	GATGAAATAC	AATGGAATCC	ACCAAGACCT	120
GAAATTAATA	AGGATGATGT	TCAACACAAG	CAAGTGTGTT	TCAGCAGAAC	ATCCTCGGGA	180
GGCTCATTGT	TGGCTTCTGA	TGTCCCAAAT	GCTCCCATAC	CTGATCT		227

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACCTGAAGGC	GGAAATTCAC	GGGGGCAGTC	TCATTAATCT	GACTTGGACA	GCTCCTGGGG	60
ATGATTATGA	CCATGGAACA	GCTCACAAGT	ATATCATTCG	AATAAGTACA	AGTATTCTTG	120
ATCTCAGAGA	CAAGTTCAAT	GAATCTCTTC	AAGTGAATAC	TACTGCTCTC	ATCCCAAAGG	180
AAGCCAACTC	TGAGGAAGTC	TTTTTGTTTA	AACCAGAAAA	CATTACTTTT	GAAAATGGCA	240
CAGATCTT						248

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

58

86220-96964060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACAGATCTTT	TCATTGCTAT	TCAGGCTGTT	GATAAGGTCG	ATCTGAAATC	AGAAATATCC	60
AACATTGCAC	GAGTATCTTT	GTTTATTCTT	CCACAGACTC	CGCCAGAGAC	ACCTAGTCCT	120
GATGAAACGT	CTGCTCCTTG	TCCTAATATT	CATA			154

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTTATTCTT	CCACAGACTC	CGCCAGAGAC	ACCTAGTCCT	GATGAAACGT	CTGCTCCTTG	60
TCCTAATATT	CATATCAACA	GCACCATTC	TGGCATTAC	ATTTTAAAAA	TTATGTGGAA	120
GTGGATAGGA	GAAGTGCAGC	TGTCAATAGC	CTAGGGCTGA	ATTTTGTGCA	GATAAATAAA	180
ATAAATCATT	CATCCTTTTT	TTTGATTATA	AAATTTTCTA	AAATGTATTT	TAGACTTCCT	240
GT						242

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCATTACACA	TTTTAAAAAT	TATGTGGAAG	TGGATAGGAG	AACTGCAGCT	GTCAATAGCC	60
TAGGGCTGAA	TTTTTGTTCAG	ATAAATAAAA	TAAATCATTC	ATCCTT		106

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAAATCACAG	GGAGATGTAC	AGCAATGGGG	CCATTTAAGA	GTTCTGTGTT	CATCTTGATT	60
CTTCACCTTC	TAGAAGGGGC	CCTGAGTAAT	TCACTCATTC	AGCTGAACAA	CAATGGCTAT	120
GAAGGCATTG	TCGTTGCAAT	CGACCCCAAT	GTGCCAGAAG	ATGAAACACT	CATTCAACAA	180
ATAAAGGACA	TGGTGACCCA	GGCATCTCTG	TATCTGTTTG	AAGCTACAGG	AAAGCGATTT	240
TATTTCAAAA	ATGTTGCCAT	TTTGATTCTT	GAAACATGGA	AGACAAAGGC	TGACTATGTG	300
AGACCAAAAC	TTGAGACCTA	CAAAAATGCT	GATGTTCTGG	TTGCTGAGTC	TACTCCTCCA	360
GGTAATGATG	AACCCTACAC	TGAGCAGATG	GGCAACTGTG	GAGAGAAGGG	TGAAAGGATC	420
CACCTCACTC	CTGATTTCAT	TGCAGGAAAA	AAGTTAGCTG	AATATGGACC	ACAAGGTAGG	480
GCATTTGTCC	ATGAGTGGGC	TCATCTACGA	TGGGGAGTAT	TTGACGAGTA	CAATAATGAT	540
GAGAAATTCT	ACTTATCCAA	TGGAAGAATA	CAAGCAGTAA	GATGTTTCAG	AGGTATTACT	600
GGTACAAATG	TAGTAAAGAA	GTGTCAGGGA	GGCAGCTGTT	ACACCAAAAAG	ATGCACATTC	660
AATAAAGTAA	CAGGACTCTA	TGAAAAAGGA	TGTGAGTTTG	TTCTCCAATC	CCGCCAGACG	720
GAGAAGGCTT	CTATAATGTT	TGCACAACAT	GTTGATTCTA	TAGTTGAATT	CTGTACAGAA	780
CAAAACCACA	ACAAAGAAGC	TCCAAACAAG	CAAAATCAAA	AATGCAATCT	CCGAAGCACA	840
TGGGAAGTGA	TCCGTGATT	TGAGGACTTT	AAGAAAACCA	CTCCTATGAC	AACACAGCCA	900
CCAAATCCCA	CCTTCTCATT	GCTGCAGATT	GGACAAAGAA	TTGTGTGTTT	AGTCCTTGAC	960

AAATCTGGAA	GCATGGCGAC	TGGTAACCGC	CTCAATCGAC	TGAATCAAGC	AGGCCAGCTT	1020
TTCCTGCTGC	AGACAGTTGA	GCTGGGGTCC	TGGGTTGGGA	TGGTGACATT	TGACAGTGCT	1080
GCCCATGTAC	AAAGTGAAC	CATACAGATA	AACAGTGGCA	GTGACAGGGA	CACACTCGCC	1140
AAAAGATTAC	CTGCAGCAGC	TTCAGGAGGG	ACGTCCATCT	GCAGCGGGCT	TCGATCGGCA	1200
TTTACTGTGA	TTAGGAAGAA	ATATCCAAC	GATGGATCTG	AAATTGTGCT	GCTGACGGAT	1260
GGGGAAGACA	ACACTATAAG	TGGGTGCTTT	AACGAGGTCA	AACAAAGTGG	TGCCATCATC	1320
CACACAGTCG	CTTTGGGGCC	CTCTGCAGCT	CAAGAACTAG	AGGAGCTGTC	CAAAATGACA	1380
GGAGGTTTAC	AGACATATGC	TTCAGATCAA	GTTTCAGAACA	ATGGCCTCAT	TGATGCTTTT	1440
GGGGCCCTTT	CATCAGGAAA	TGGAGCTGTC	TCTCAGCGCT	CCATCCAGCT	TGAGAGTAAG	1500
GGATTAACCC	TCCAGAACAG	CCAGTGGATG	AATGGCACAG	TGATCGTGGA	CAGCACCGTG	1560
GGAAAGGACA	CTTTGTTTCT	TATCACCTGG	ACAACGCAGC	CTCCCCAAAT	CCTTCTCTGG	1620
GATCCCAAGT	GACAGAAGCA	AGGTGGCTTT	GATGTGGACA	AAAAACACCA	AATGGCCTAC	1680
CTCCAAATCC	CAGGCATTGC	TAAGGTTGGC	ACTTGGAAT	ACAGTCTGCA	AGCAAGCTCA	1740
CAAACCTTGA	CCCTGACTGT	CACGTCCCGT	GCGTCCAATG	CTACCCTGCC	TCCAATTACA	1800
GTGACTTCCA	AAACGAACAA	GGACACCAGC	AAATTCCCCA	GCCCTCTGGT	AGTTTATGCA	1860
AATATTTCGCC	AAGGAGCCTC	CCCAATTCTC	AGGGCCAGTG	TCACAGCCCT	GATTGAATCA	1920
GTGAATGGAA	AAACAGTTAC	CTTGGAAC	CTGGATAATG	GAGCAGGTGC	TGATGCTACT	1980
AAGGATGACG	GTGTCTACTC	AAGGTATTTT	ACAACCTATG	ACACGAATGG	TAGATACAGT	2040
GTAAGAGTGC	GGGCTCTGGG	AGGAGTTAAC	GCAGCCAGAC	GGAGAGTGAT	ACCCAGCAG	2100
AGTGGAGCAC	TGTACATACC	TGGCTGGATT	GAGAATGATG	AAATACAATG	GAATCCACCA	2160
AGACCTGAAA	TTAATAAGGA	TGATGTTCAA	CACAAGCAAG	TGTGTTTCAG	CAGAACATCC	2220
TCGGGAGGCT	CATTGTGGC	TTCTGATGTC	CCAAATGCTC	CCATACCTGA	TCTCTTCCCA	2280
CCTGGCCAAA	TCACCGACCT	GAAGGCGGAA	ATTCACGGGG	GCAGTCTCAT	TAATCTGACT	2340
TGGACAGCTC	CTGGGGATGA	TTATGACCAT	GGAACAGCTC	ACAAGTATAT	CATTCTGAATA	2400
AGTACAAGTA	TTCTTGATCT	CAGAGACAAG	TTCAATGAAT	CTCTTCAAGT	GAATACTACT	2460
GCTCTCATCC	CAAAGGAAGC	CAACTCTGAG	GAAGTCTTTT	TGTTTAAACC	AGAAAACATT	2520
ACTTTTGAAA	ATGGCACAGA	TCTTTTCATT	GCTATTTCAGG	CTGTTGATAA	GGTCGATCTG	2580
AAATCAGAAA	TATCCAACAT	TGCACGAGTA	TCTTTGTTTA	TTCTTCCACA	GACTCCGCCA	2640
GAGACACCTA	GTCCTGATGA	AACGTCTGCT	CCTTGTCCTA	ATATTTCATAT	CAACAGCACC	2700
ATTCTGCGCA	TTCACATTTT	AAAAATTATG	TGGAAGTGGA	TAGGAGAACT	GCAGCTGTCA	2760
ATAGCCTAGG	GCTGAATTTT	TGTCAGATAA	ATAAAATAAA	TCATTTCATCC	TTA	2813

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AACAAAGTGG	TGCCATCATC	CACACAGTCG	CTTTGGGGCC	CTCTGCAGCT	CAAGAACTAG	60
AGGAGCTGTC	CAAAATGACA	GGAGGTTTAC	AGACATATGC	TTCAGATCAA	GTTCAGAACA	120
ATGGCCTCAT	TGATGCTTTT	GGGGCCCTTT	CATCAGGAAA	TGGAGCTGTC	TCTCAGCGCT	180
CCATCCAGCT	TGAGAGTAAG	GGATTAACCC	TCCAGAACAG	CCAGTGGATG	AATGGCACAG	240
TGATCGTGGA	CAGCACCGTG	GGAAAGGACA	CTTTGTTTCT	TATCACCTGG	ACAACGCAGC	300
CTCCCCAAAT	CCTTCTCTGG	GATCCCAGTG	GACAGAAGCA	AGGTGGCTTT	GATGTGGACA	360
AAAAACACCA	AATGGCCTAC	CTCCAAATCC	CAGGCATTGC	TAAGGTTGGC	ACTTGGAAT	420
ACAGTCTGCA	AGCAAGCTCA	CAAACCTTGA	CCCTGACTGT	CACGTCCCGT	GCGTCCAATG	480
CTACCCTGCC	TCCAATTACA	GTGACTTCCA	AAACGAACAA	GGACACCAGC	AAATTCCCCA	540
GCCCTCTGGT	AGTTTATGCA	AATATTTCGCC	AAGGAGCCTC	CCCAATTCTC	AGGGCCAGTG	600
TCACAGCCCT	GATTGAATCA	GTGAATGGAA	AAACAGTTAC	CTTGGAAC	CTGGATAATG	660
GAGCAGGTGC	TGATGCTACT	AAGGATGACG	GTGTCTACTC	AAGGTATTTT	ACAACCTTATG	720
ACACGAATGG	TAGATACAGT	GTAAGAGTGC	GGGCTCTGGG	AGGAGTTAAG	GACGCCAGAC	780
GGAGAGTGAT	ACCCAGCAG	AGTGGAGCAC	TGTACATACC	TGGCTGGATT	GAGAATGATG	840
AAATACAATG	GAATCCACCA	AGACCTGAAA	TTAATAAGGA	TGATGTTCAA	CACAAGCAAG	900
TGTGTTTCAG	CAGAACATCC	TCGGGAGGCT	CATTGTGGC	TTCTGATGTC	CCAAATGCTC	960
CCATCAATGA	TCTCTTCCCA	CCTGGCCAAA	TCACCGACCT	GAAGGCGGAA	ATTACCGGGG	1020
GCAGTCTCAT	TAATCTGACT	TGGACAGCTC	CTGGGGATGA	TTATGACCAT	GGAACAGCTC	1080
ACAAGTATAT	CATTCTGAATA	AGTACAAGTA	TTCTTGATCT	CAGAGACAAG	TTCAATGAAT	1140
CTCTTCAAGT	GAATACTACT	GCTCTCATCC	CAAAGGAAGC	CAACTCTGAG	GAAGTCTTTT	1200
TGTTTAAACC	AGAAAACATT	ACTTTTGAAA	ATGGCACAGA	TCTTTTCATT	GCTATTTCAGG	1260
CTGTTGATAA	GGTCGATCTG	AAATCAGAAA	TATCCAACAT	TGCACGAGTA	TCTTTGTTTA	1320
TTCTTCCACA	GACTCCGCCA	GAGACACCTA	GTCCTGATGA	AACGTCTGCT	CCTTGTCCTA	1380

ATATTCATAT	CAACAGCACC	ATTCCTGGCA	TTCACATTTT	AAAAATTATG	TGGAAGTGGA	1440
TAGGAGAACT	GCAGCTGTCA	ATAGCCTAGG	GCTGAATTTT	TGTCAGATAA	ATAAAATAAA	1500
TCATTCATCC	TTTTTTTGA	TTATAAAATT	TTCTAAAATG	TATTTTAGAC	TTCCTGTAGG	1560
GGCGATATA	CTAAATGTAT	ATAGTACATT	TATACTAAAT	GTATTCCTGT	AGGGGGCGAT	1620
ATACTAAATG	TATTTTAGAC	TTCCTGTAGG	GGGCGATAAA	ATAAAATGCT	AAACAACCTGG	1680
GTA						1683

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2983 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAAATCACAG	GGAGATGTAC	AGCAATGGGG	CCATTTAAGA	GTTCTGTGTT	CATCTTGATT	60
CTTCACCTTC	TAGAAGGGGC	CCTGAGTAAT	TCACTCATT	AGCTGAACAA	CAATGGCTAT	120
GAAGGCATTG	TCGTTGCAAT	CGACCCCAAT	GTGCCAGAAG	ATGAAACACT	CATTCAACAA	180
ATAAAGGACA	TGGTGACCCA	GGCATCTCTG	TATCTGTTTG	AAGCTACAGG	AAAGCGATT	240
TATTTCAAAA	ATGTTGCCAT	TTTGATTCCCT	GAAACATGGA	AGACAAAGGC	TGACTATGTG	300
AGACCAAAAC	TTGAGACCTA	CAAAAATGCT	GATGTTCTGG	TTGCTGAGTC	TACTCCTCCA	360
GGTAATGATG	AACCCTACAC	TGAGCAGATG	GGCAACTGTG	GAGAGAAGGG	TGAAAGGATC	420
CACCTCACTC	CTGATTTTCAT	TGCAGGAAAA	AAGTTAGCTG	AATATGGACC	ACAAGGTAGG	480
GCATTTGTCC	ATGAGTGGGC	TCATCTACGA	TGGGGAGTAT	TTGACGAGTA	CAATAATGAT	540
GAGAAATTCT	ACTTATCCAA	TGGAAGAATA	CAAGCAGTAA	GATGTTTCAGC	AGGTATTACT	600
GGTACAAATG	TAGTAAAGAA	GTGTCAGGGA	GGCAGCTGTT	ACACCAAAAG	ATGCACATTC	660
AATAAAGTAA	CAGGACTCTA	TGAAAAAGGA	TGTGAGTTTG	TTCTCCAATC	CCGCCAGACG	720
GAGAAGGCTT	CTATAATGTT	TGCACAACAT	GTTGATTCTA	TAGTTGAATT	CTGTACAGAA	780
CAAAACCACA	AAAAGTAAAG	TCCAACAACG	AATGCAATCT	CCGAAGCACA		840
TGGGAAGTGA	TCCGTGATT	TGAGGACTTT	AAGAAAACCA	CTCCTATGAC	AACACAGCCA	900
CCAAATCCCA	CCTTCTCATT	GCTGCAGATT	GGACAAAGAA	TTGTGTGTTT	AGTCCTTGAC	960
AAATCTGGAA	GCATGGCGAC	TGGTAACCGC	CTCAATCGAC	TGAATCAAGC	AGGCCAGCTT	1020
TTCTCTGCTG	AGACAGTTGA	GCTGGGGTCC	TGGGTTGGGA	TGGTGACATT	TGACAGTGCT	1080
GCCCATGTAC	AAAGTGAAC	CATACAGATA	AACAGTGGCA	GTGACAGGGA	CACACTCGCC	1140
AAAAGATTAC	CTGCAGCAGC	TTCAGGAGGG	ACGTCCATCT	GCAGCGGGCT	TCGATCGGCA	1200
TTTACTGTGA	TTAGGAAGAA	ATATCCAAC	GATGGATCTG	AAATTGTGCT	GCTGACGGAT	1260
GGGGAAGACA	ACACTATAAG	TGGGTGCTTT	AACGAGGTCA	AACAAAGTGG	TGCCATCATC	1320
CACACAGTCG	CTTTGGGGCC	CTCTGCAGCT	CAAGAAGTGA	AGGAGCTGTC	CAAAATGACA	1380
GGAGGTTTAC	AGACATATGC	TTCAGATCAA	GTTTCAGAAC	ATGGCCTCAT	TGATGCTTTT	1440
GGGGCCCTTT	CATCAGGAAA	TGGAGCTGTC	TCTCAGCGCT	CCATCCAGCT	TGAGAGTAAG	1500
GGATTAACCC	TCCAGAACAG	CCAGTGGATG	AATGGCACAG	TGATCGTGGA	CAGCACCGTG	1560
GGAAAGGACA	CTTTGTTTCT	TATCACCTGG	ACAACGCAGC	CTCCCCAAAT	CCTTCTCTGG	1620
GATCCCAGTG	GACAGAAGCA	AGGTGGCTTT	GTAGTGGACA	AAAACACCAA	AATGGCCTAC	1680
CTCCAAATCC	CAGGCATTGC	TAAGGTTGGC	ACTTGGAAT	ACAGTCTGCA	AGCAAGCTCA	1740
CAAACCTTGA	CCCTGACTGT	CACGTCCCCT	GCGTCCAATG	CTACCCTGCC	TCCAATTACA	1800
GTGACTTCCA	AAACGAACAA	GGACACCAGC	AAATTCCCCA	GCCCTCTGGT	AGTTTATGCA	1860
AATATTGCGC	AAGGAGCCTC	CCCAATTCTC	AGGGCCAGTG	TCACAGCCCT	GATTGAATCA	1920
GTGAATGGAA	AAACAGTTAC	CTTGGAACCTA	CTGGATAATG	GAGCAGGTGC	TGATGCTACT	1980
AAGGATGACG	GTGTCTACTC	AAGGTATTTT	ACAACCTTATG	ACACGAATGG	TAGATACAGT	2040
GTAAAAGTGC	GGGCTCTGGG	AGGAGTTAAT	GCAGCCAGAC	GGAGAGTGAT	ACCCACAGCAG	2100
AGTGAGGAC	TGTACATACC	TGGCTGGATT	GAGAATGATG	AAATACAATG	GAATCCACCA	2160
AGACCTGAAA	TTAATAAGGA	TGATGTTCAA	CACAAGCAAG	TGTGTTTCAG	CAGAACATCC	2220
TCGGGAGGCT	CATTTGTGGC	TTCTGATGTC	CCAAATGCTC	CCATACCTGA	TCTCTTCCCA	2280
CCTGGCCAAA	TCACCGACCT	GAAGGCGGAA	ATTCACGGGG	GCAGTCTCAT	TAATCTGACT	2340
TGGACAGCTC	CTGGGGATGA	TTATGACCAT	GGAACAGCTC	ACAAGTATAT	CATTTCGAATA	2400
AGTACAAGTA	TTCTTGATCT	CAGAGACAAG	TTCAATGAAT	CTCTTCAAGT	GAATACTACT	2460
GCTCTCATCC	CAAAGGAAGC	CAACTCTGAG	GAAGTCTTTT	TGTTTAAACC	AGAAAACATT	2520
ACTTTTGAAA	ATGGCACAGA	TCTTTTCATT	GCTATTTCAGG	CTGTTGATAA	GGTCGATCTG	2580
AAATCAGAAA	TATCCAACAT	TGCACGAGTA	TCTTTGTTTA	TTCTCCACA	GACTCCGCCA	2640
GAGACACCTA	GTCCTGATGA	AACGTCTGCT	CCTTGTCCTA	ATATTCATAT	CAACAGCACC	2700
ATTCCTGGCA	TTCACATTTT	AAAAATTATG	TGGAAGTGGG	TAGGAGAACT	GCAGCTGTCA	2760
ATAGCCTAGG	GCTGAATTTT	TGTCAGATAA	ATAAAATGAA	TCATTCATCC	TTTTTTTTGA	2820
TTATAAAATT	TTCTAAAATG	TATTTTAGAC	TTCCTGTAGG	GGGCGATATA	CTAAATGTAT	2880

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ATAGTACATT TATACTAAAT GTATTCCTGT AGGGGGCGAT ATACTAAATG TATTTTAGAC 2940
TTCCTGTAGG GGGCGATAAA ATAAAATGCT AAACAACCTGG GTA 2983

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC 60
CGGGAATT 68

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60
GAATTCCG 68

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAAGCAAGGT GGCTTTGTAG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAGCTCACAA ACCTTGACCC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACAGTGTA AAGTGCGGGC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTGGGGATG ATTATGACCA

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACGTCTGCTC CTTGTCCTAA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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GCAGACGTTT CATCAGGACT

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGGGAAGAGA TCAGGTATGG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGAGCCCGC ACTTTTACAC

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACAGTCAGGG TCAAGGTTTG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTGGAGGGTT AATCCCTTAC

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCTATGACA ACACAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GATGTTCTGG TTGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCTGTGTTG TCATAGGAGT G

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGTTCATCAT TACCTGGAGG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCACCTCAC TCCTGATTTC ATTGC

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGATTCAGTC GATTGAGGCG GTTAC

25

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Gly	Pro	Phe	Lys	Ser	Ser	Val	Phe	Ile	Leu	Ile	Leu	His	Leu	Leu
1				5				10					15		
Glu	Gly	Ala	Leu	Ser	Asn	Ser	Leu	Ile	Gln	Leu	Asn	Asn	Asn	Gly	Tyr
		20						25				30			
Glu	Gly	Ile	Val	Val	Ala	Ile	Asp	Pro	Asn	Val	Pro	Glu	Asp	Glu	Thr
		35					40					45			
Leu	Ile	Gln	Gln	Ile	Lys	Asp	Met	Val	Thr	Gln	Ala	Ser	Leu	Tyr	Leu
	50				55					60					
Phe	Glu	Ala	Thr	Gly	Lys	Arg	Phe	Tyr	Phe	Lys	Asn	Val	Ala	Ile	Leu
65				70					75					80	
Ile	Pro	Glu	Thr	Trp	Lys	Thr	Lys	Ala	Asp	Tyr	Val	Arg	Pro	Lys	Leu
			85					90					95		
Glu	Thr	Tyr	Lys	Asn	Ala	Asp	Val	Leu	Val	Ala	Glu	Ser	Thr	Pro	Pro
			100					105					110		
Gly	Asn	Asp	Glu	Pro	Tyr	Thr	Glu	Gln	Met	Gly	Asn	Cys	Gly	Glu	Lys
		115					120					125			
Gly	Glu	Arg	Ile	His	Leu	Thr	Pro	Asp	Phe	Ile	Ala	Gly	Lys	Lys	Leu
	130					135					140				
Ala	Glu	Tyr	Gly	Pro	Gln	Gly	Arg	Ala	Phe	Val	His	Glu	Trp	Ala	His
145					150					155					160
Leu	Arg	Trp	Gly	Val	Phe	Asp	Glu	Tyr	Asn	Asn	Asp	Glu	Lys	Phe	Tyr
			165					170						175	
Leu	Ser	Asn	Gly	Arg	Ile	Gln	Ala	Val	Arg	Cys	Ser	Ala	Gly	Ile	Thr
		180						185					190		
Gly	Thr	Asn	Val	Val	Lys	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Tyr	Thr	Lys
		195					200					205			
Arg	Cys	Thr	Phe	Asn	Lys	Val	Thr	Gly	Leu	Tyr	Glu	Lys	Gly	Cys	Glu
	210					215					220				
Phe	Val	Leu	Gln	Ser	Arg	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Ala
225					230					235					240
Gln	His	Val	Asp	Ser	Ile	Val	Glu	Phe	Cys	Thr	Glu	Gln	Asn	His	Asn
			245					250						255	
Lys	Glu	Ala	Pro	Asn	Lys	Gln	Asn	Gln	Lys	Cys	Asn	Leu	Arg	Ser	Thr
		260						265					270		
Trp	Glu	Val	Ile	Arg	Asp	Ser	Glu	Asp	Phe	Lys	Lys	Thr	Thr	Pro	Met
		275					280						285		
Thr	Thr	Gln	Pro	Pro	Asn	Pro	Thr	Phe	Ser	Leu	Leu	Gln	Ile	Gly	Gln
	290					295						300			
Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly	Ser	Met	Ala	Thr	Gly
305					310					315					320
Asn	Arg	Leu	Asn	Arg	Leu	Asn	Gln	Ala	Gly	Gln	Leu	Phe	Leu	Leu	Gln
			325						330					335	
Thr	Val	Glu	Leu	Gly	Ser	Trp	Val	Gly	Met	Val	Thr	Phe	Asp	Ser	Ala
		340						345					350		
Ala	His	Val	Gln	Ser	Glu	Leu	Ile	Gln	Ile	Asn	Ser	Gly	Ser	Asp	Arg
		355					360					365			
Asp	Thr	Leu	Ala	Lys	Arg	Leu	Pro	Ala	Ala	Ala	Ser	Gly	Gly	Thr	Ser
	370					375						380			
Ile	Cys	Ser	Gly	Leu	Arg	Ser	Ala	Phe	Thr	Val	Ile	Arg	Lys	Lys	Tyr
385					390					395					400
Pro	Thr	Asp	Gly	Ser	Glu	Ile	Val	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn
				405					410					415	

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Thr	Ile	Ser	Gly	Cys	Phe	Asn	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Ile		
			420					425					430				
His	Thr	Val	Ala	Leu	Gly	Pro	Ser	Ala	Ala	Gln	Glu	Leu	Glu	Glu	Leu		
		435					440					445					
Ser	Lys	Met	Thr	Gly	Gly	Leu	Gln	Thr	Tyr	Ala	Ser	Asp	Gln	Val	Gln		
	450					455					460						
Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Ser	Ser	Gly	Asn	Gly		
465					470					475					480		
Ala	Val	Ser	Gln	Arg	Ser	Ile	Gln	Leu	Glu	Ser	Lys	Gly	Leu	Thr	Leu		
				485					490					495			
Gln	Asn	Ser	Gln	Trp	Met	Asn	Gly	Thr	Val	Ile	Val	Asp	Ser	Thr	Val		
			500					505					510				
Gly	Lys	Asp	Thr	Leu	Phe	Leu	Ile	Thr	Trp	Thr	Thr	Gln	Pro	Pro	Gln		
	515						520					525					
Ile	Leu	Leu	Trp	Asp	Pro	Ser	Gly	Gln	Lys	Gln	Gly	Gly	Phe	Val	Val		
	530					535					540						
Asp	Lys	Asn	Thr	Lys	Met	Ala	Tyr	Leu	Gln	Ile	Pro	Gly	Ile	Ala	Lys		
545					550					555					560		
Val	Gly	Thr	Trp	Lys	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Gln	Thr	Leu	Thr		
				565					570					575			
Leu	Thr	Val	Thr	Ser	Arg	Ala	Ser	Asn	Ala	Thr	Leu	Pro	Pro	Ile	Thr		
			580					585					590				
Val	Thr	Ser	Lys	Thr	Asn	Lys	Asp	Thr	Ser	Lys	Phe	Pro	Ser	Pro	Leu		
		595					600					605					
Val	Val	Tyr	Ala	Asn	Ile	Arg	Gln	Gly	Ala	Ser	Pro	Ile	Leu	Arg	Ala		
	610				615						620						
Ser	Val	Thr	Ala	Leu	Ile	Glu	Ser	Val	Asn	Gly	Lys	Thr	Val	Thr	Leu		
625					630					635					640		
Glu	Leu	Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ala	Thr	Lys	Asp	Asp	Gly		
				645					650					655			
Val	Tyr	Ser	Arg	Tyr	Phe	Thr	Thr	Tyr	Asp	Thr	Asn	Gly	Arg	Tyr	Ser		
			660					665					670				
Val	Lys	Val	Arg	Ala	Leu	Gly	Gly	Val	Asn	Ala	Ala	Arg	Arg	Arg	Val		
		675					680					685					
Ile	Pro	Gln	Gln	Ser	Gly	Ala	Leu	Tyr	Ile	Pro	Gly	Trp	Ile	Glu	Asn		
	690					695					700						
Asp	Glu	Ile	Gln	Trp	Asn	Pro	Pro	Arg	Pro	Glu	Ile	Asn	Lys	Asp	Asp		
705					710					715					720		
Val	Gln	His	Lys	Gln	Val	Cys	Phe	Ser	Arg	Thr	Ser	Ser	Gly	Gly	Ser		
				725					730					735			
Phe	Val	Ala	Ser	Asp	Val	Pro	Asn	Ala	Pro	Ile	Pro	Asp	Leu	Phe	Pro		
			740					745					750				
Pro	Gly	Gln	Ile	Thr	Asp	Leu	Lys	Ala	Glu	Ile	His	Gly	Gly	Ser	Leu		
			755				760					765					
Ile	Asn	Leu	Thr	Trp	Thr	Ala	Pro	Gly	Asp	Asp	Tyr	Asp	His	Gly	Thr		
	770					775					780						
Ala	His	Lys	Tyr	Ile	Ile	Arg	Ile	Ser	Thr	Ser	Ile	Leu	Asp	Leu	Arg		
785					790					795					800		
Asp	Lys	Phe	Asn	Glu	Ser	Leu	Gln	Val	Asn	Thr	Thr	Ala	Leu	Ile	Pro		
			805						810					815			
Lys	Glu	Ala	Asn	Ser	Glu	Glu	Val	Phe	Leu	Phe	Lys	Pro	Glu	Asn	Ile		
			820					825					830				
Thr	Phe	Glu	Asn	Gly	Thr	Asp	Leu	Phe	Ile	Ala	Ile	Gln	Ala	Val	Asp		
			835				840					845					
Lys	Val	Asp	Leu	Lys	Ser	Glu	Ile	Ser	Asn	Ile	Ala	Arg	Val	Ser	Leu		
	850					855					860						
Phe	Ile	Pro	Pro	Gln	Thr	Pro	Pro	Glu	Thr	Pro	Ser	Pro	Asp	Glu	Thr		
865					870					875					880		
Ser	Ala	Pro	Cys	Pro	Asn	Ile	His	Ile	Asn	Ser	Thr	Ile	Pro	Gly	Ile		
				885					890					895			
His	Ile	Leu	Lys	Ile	Met	Trp	Lys	Trp	Ile	Gly	Glu	Leu	Gln	Leu	Ser		
			900					905					910				
Ile	Ala																

(2) INFORMATION FOR SEQ ID NO:42:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Tyr	Asn	Asn	Asp	Glu	Lys	Phe	Tyr	Leu	Ser	Asn	Gly	Arg	Ile	Gln	Ala
1				5				10						15	
Val	Arg	Cys													

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Tyr	Thr	Lys	Arg	Cys	Thr	Phe	Asn	Lys	Val	Thr	Gly	Leu	Tyr	Glu	Lys
1				5				10						15	
Gly	Cys	Glu	Phe	Val	Leu	Gln	Ser								
				20											

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asn	Ser	Gly	Ser	Asp	Arg	Asp	Thr	Leu	Ala	Lys	Arg	Leu	Pro	Ala	Ala
1				5				10						15	
Ala	Ser	Gly	Gly												
				20											

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr	Trp	Thr	Thr	Gln	Pro	Pro	Gln	Ile	Leu	Leu	Trp	Asp	Pro	Ser	Gly
1				5				10						15	
Gln	Lys	Gln	Gly	Phe	Val	Val	Asp	Lys	Asn	Thr	Lys				
				20			25								

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03049696.032798

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ile	Thr	Val	Thr	Ser	Lys	Thr	Asn	Lys	Asp	Thr	Ser	Lys	Phe	Pro	Ser
1				5				10						15	
Pro	Leu	Val	Val	Tyr	Ala	Asn	Ile	Arg	Gln	Gly	Ala	Ser			
			20					25							

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ala	Thr	Lys	Asp	Asp	Gly	Val	Tyr	Ser
1				5				10						15	
Arg	Tyr	Phe	Thr	Thr	Tyr	Asp	Thr	Asn	Gly	Arg	Tyr	Ser	Val	Lys	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Trp	Ile	Glu	Asn	Asp	Glu	Ile	Gln	Trp	Asn	Pro	Pro	Arg	Pro	Glu	Ile
1				5				10						15	
Asn	Lys	Asp	Asp	Val	Gln	His	Lys	Gln	Val	Cys	Phe	Ser	Arg	Thr	Ser
			20					25					30		
Ser	Gly	Gly													
			35												

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

99

00049696-032700

Glu Ile Asn Lys Asp Asp Val Gln His Lys Gln Val Cys Phe Ser Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20

00045696-032793